

1/8

SEQUENCE LISTING

<110> ASAHI KASEI KABUSHIKI KAISHA
TAKAHASHI, Tsuneo
ONO, Mitsuhiro
ISHIMARU, Hiroshi
KANNO, Kimiyoshi
TAKAHASHI, Chiaki

<120> Novel receptor protein and method for the diagnosis of an inflammatory disease by using the same

<130> 99-1043

<150> JP 10-249752

<151> 1998-09-03

<150> JP 11-070800

<151> 1999-03-16

<150> PCT/JP99/04801

<151> 1999-09-03

<160> 12

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<211> 1014

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1011)

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tgc gac cgc cct gtg gac tgc ctg gat ggc gcc tgc ctg gcc atc gac 96
Ser Asp Arg Pro Val Asp Cys Leu Asp Gly Ala Cys Leu Ala Ile Asp
20 25 30

ccg ctg cgc gtg gcc ccg ctc cca ctg taa gcc gac atc ttc ctg gtg 144
Pro Leu Arg Val Ala Pro Leu Pro Leu Tyr Ala Ala Ile Phe Leu Val
35 40 45

ggg gtg ccg ggc aat gcc atg gtg gcc tgg gtg gct ggg aag gtg gcc 192
Gly Val Pro Gly Asn Ala Met Val Ala Trp Val Ala Gly Lys Val Ala
50 55 60

09/786442-050501

cgc	cg	agg	gt	g	gt	g	cc	acc	tgg	ttg	ctc	cac	ctg	g	cc	gt	g	cg	g	at	240
Arg	Arg	Arg	Arg	Val	Gly	Ala	Thr	Trp	Leu	Leu	His	Leu	Ala	Val	Ala	Asp					
65				70					75					80							
ttg	ctg	tgc	tgt	ttg	tct	ctg	ccc	atc	ctg	gca	gt	cc	att	g	cc	cg	g	at	288		
Leu	Leu	Cys	Cys	Leu	Ser	Leu	Pro	Ile	Leu	Ala	Val	Pro	Ile	Ala	Arg						
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gga	ggc	cac	tgg	ccg	tat	ggt	gca	gt	ggc	tgt	cg	g	cc	cc	336						
Gly	Gly	His	Trp	Pro	Tyr	Gly	Ala	Val	Gly	Cys	Arg	Ala	Leu	Pro	Ser						
100				105					105					110							
atc	atc	ctg	ctg	acc	atg	tat	g	cc	agc	gt	ctg	c	c	ctg	gca	g	ct	ct	ct	ct	384
Ile	Ile	Leu	Leu	Thr	Met	Tyr	Ala	Ser	Val	Leu	Leu	Ala	Leu								
115				120										125							
agt	gcc	gac	ctc	tgc	t	tc	ctg	gct	ctc	gg	cc	g	cc	tgg	tgg	tct	ac	432			
Ser	Ala	Asp	Leu	Cys	Phe	Leu	Ala	Leu	Gly	Pro	Ala	Trp	Trp	Ser	Thr						
130				135										140							
gtt	cag	cg	gc	tg	gg	gt	cg	gt	gg	gt	gg	g	cc	tgg	tgg	aca	480				
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145				150					155					160							
ctg	g	cc	tt	ct	cc	acc	gt	cc	cc	g	cc	at	ac	cg	cg	ct	ac	528			
Leu	Ala	Leu	Leu	Leu	Thr	Val	Pro	Ser	Ala	Ile	Tyr	Arg	Arg	Leu	His						
165				170										175							
cag	gag	cac	tt	cc	g	cc	ct	cg	c	tg	tg	g	ac	ta	gg	gg	576				
Gln	Glu	His	Phe	Pro	Ala	Arg	Leu	Gln	Cys	Val	Val	Asp	Tyr	Gly							
180				185										190							
tcc	tcc	agc	acc	gag	aat	g	cc	tg	ac	t	cc	at	cg	tt	tt	tt	gg	624			
Ser	Ser	Ser	Ser	Thr	Glu	Asn	Ala	Val	Thr	Ala	Ile	Arg	Phe	Leu	Phe	Gly					
195				200										205							
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Phe	Leu	Gly	Pro	Leu	Val	Ala	Val	Ala	Ser	Cys	His	Ser	Ala	Leu	Leu						
210				215										220							
tgc	tgg	gca	gc	cg	tg	cg	cc	ct	g	cc	ac	g	cc	at	tg	tg	720				
Cys	Trp	Ala	Ala	Arg	Arg	Cys	Arg	Pro	Leu	Gly	Thr	Ala	Ile	Val	Val						
225				230					235					240							
ggg	ttt	ttt	gt	tg	gca	cc	ta	ca	ct	tg	cc	tg	cc	tt	tg	cc	768				
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Thr	Val	Ala	Ala	Pro	Asn	Ser	Ala	Leu	Leu	Ala	Arg	Ala	Leu	Arg	Ala						
260				265										270							
gaa	cc	c	at	g	g	g	cc	ct	g	ct	ca	ag	tg	ct	cc	aa	cc	864			
Glu	Pro	Leu	Ile	Val	Gly	Leu	Ala	Leu	Ala	His	Ser	Cys	Leu	Asn	Pro						
275				280										285							
atg	ct	tc	ct	tg	ta	tt	gg	ag	g	ct	ca	ct	cg	cc	tg	cc	912				
Met	Leu	Phe	Leu	Tyr	Phe	Gly	Arg	Ala	Gln	Leu	Arg	Arg	Ser	Leu	Pro						
290				295					300												
gct	g	cc	t	gt	ca	c	tg	g	cc	tg	ag	g	cc	c	ag	gt	960				
Ala	Ala	Cys	His	Trp	Ala	Leu	Arg	Glu	Ser	Gln	Gly	Gln	Asp	Glu	Ser						

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gtg gac agc aag aaa tcc acc agc cat gac ctg gtc tcg gag atg gag				1008
Val Asp Ser Lys Lys Ser Thr Ser His Asp Leu Val Ser Glu Met Glu				
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Val				

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 35 40 45
 Gly Val Pro Gly Asn Ala Met Val Ala Trp Val Ala Gly Lys Val Ala
 50 55 60
 Arg Arg Arg Val Gly Ala Thr Trp Leu Leu His Leu Ala Val Ala Asp
 65 70 75 80
 Leu Leu Cys Cys Leu Ser Leu Pro Ile Leu Ala Val Pro Ile Ala Arg
 85 90 95
 Gly Gly His Trp Pro Tyr Gly Ala Val Gly Cys Arg Ala Leu Pro Ser
 100 105 110
 Ile Ile Leu Leu Thr Met Tyr Ala Ser Val Leu Leu Ala Ala Leu
 115 120 125
 Ser Ala Asp Leu Cys Phe Leu Ala Leu Gly Pro Ala Trp Trp Ser Thr
 130 135 140
 Val Gln Arg Ala Cys Gly Val Gln Val Ala Cys Gly Ala Ala Trp Thr
 145 150 155 160
 Leu Ala Leu Leu Leu Thr Val Pro Ser Ala Ile Tyr Arg Arg Leu His
 165 170 175
 Gln Glu His Phe Pro Ala Arg Leu Gln Cys Val Val Asp Tyr Gly Gly
 180 185 190
 Ser Ser Ser Thr Glu Asn Ala Val Thr Ala Ile Arg Phe Leu Phe Gly
 195 200 205
 Phe Leu Gly Pro Leu Val Ala Val Ala Ser Cys His Ser Ala Leu Leu
 210 215 220
 Cys Trp Ala Ala Arg Arg Cys Arg Pro Leu Gly Thr Ala Ile Val Val
 225 230 235 240
 Gly Phe Phe Val Cys Trp Ala Pro Tyr His Leu Leu Gly Leu Val Leu
 245 250 255
 Thr Val Ala Ala Pro Asn Ser Ala Leu Leu Ala Arg Ala Leu Arg Ala

260	265	270	
Glu Pro Leu Ile Val Gly Leu Ala Leu Ala His Ser Cys Leu Asn Pro			
275	280	285	
Met Leu Phe Leu Tyr Phe Gly Arg Ala Gln Leu Arg Arg Ser Leu Pro			
290	295	300	
Ala Ala Cys His Trp Ala Leu Arg Glu Ser Gln Gly Gln Asp Glu Ser			
305	310	315	320
Val Asp Ser Lys Lys Ser Thr Ser His Asp Leu Val Ser Glu Met Glu			
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Val			

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〈211〉 1287

<212> DNA

<213> Homo sapiens

<400> 3

<210> 4

〈211〉 1287

<212> DNA

〈213〉 *Homo sapiens*

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ttagctcct	ggatccagct	atgccttgaag	ccagtcgttgt	gaaatgagat	aagaagatac	180
acacccacaa	tgtctctcca	gccttacaccc	ccatctccga	gaccaggcgt	ggcttgggtgg	240
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cagaatgttgc	ccccatccat	gttccatgggtt	tcttgcgttgcgtt	tgggatgttgcgtt	tgggatgttgcgtt	1260
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<212> DNA

<213> Artificial Sequence

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<221> modified base

<222> 18

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<221> modified base

<222> 22

<223> i

<220>

<221> modified base

<222> 24

<223> i

<220>

<223> Degenerative PCR primer designed based on the seq of conventional

7-pass transmembrane receptor proteins which are considered to participate in the proliferation of melanoma

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atcttaagct tgaacctngc ctnngcdgac

30

<210> 6

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<221> misc difference

<222> 21

<223> a, g, c or t

<220>

<221> modified base

<222> 22

<223> i

<220>

<221> modified base

<222> 28

<223> i

<220>

<223> Degenerative PCR primer designed based on the seq of conventional 7-pass transmembrane receptor proteins which are considered to participate in the proliferation of melanoma

<400> 6

cccaacgaat tcrtiagaisa nnggrtinav rca

33

<210> 7

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer used for constructing the recombinant DNA containing C5L2 gene; primer has a seq obtained by adding spacer gggg and *Hind*III site aagctt to the 5'-end of a 22-nucleotide seq corresponding to the 1st (a) to 22nd (t) of SEQ ID NO:1

<400> 7
 gggagaagctt atggggaaacg attctgtcag ct 32

<210> 8
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic primer used for constructing the recombinant DNA containing C5L2 gene; primer has a seq obtained by adding spacer ggaa and SacII site ccgcgg to the 5'-end of a 20-nucleotide seq corresponding to the 206th (c) to 225th (a) of SEQ ID NO:4

<400> 8
 gggaccgcgg caccctccatc tccgagacca 30

<210> 9
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic primer used in RT-PCR performed for amplifying C5L2 gene

<400> 9
 atcatccatgc tgaccatgtia tgccag 26

<210> 10
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic primer used in RT-PCR performed for amplifying C5L2 gene

<400> 10
 aaccggatgg cagtcaccgc attct 25

<210> 11

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer used in RT-PCR performed for amplifying G3PDH
(glyceraldehyde 3-phosphate dehydrogenase) gene

<400> 11

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26

<210> 12

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer used in RT-PCR performed for amplifying G3PDH
(glyceraldehyde 3-phosphate dehydrogenase) gene

<400> 12

catgaggccc atgaggccca ccac

24

09786444-030001